

AMENDMENT TO THE SPECIFICATION

Please amend the specification as shown:

Please delete the paragraph on page 10, lines 6-8, and replace it with the following paragraph:

FIGURE 6 contains TABLE 1, which provides among other things a variety of data and other information on UDP-N-acetylmuramoylalanine-D-glutamate ligase (*murD*) from *S. aureus*. The primers are disclosed as SEQ ID NOS 10-23 and the peptides are disclosed as SEQ ID NOS 326-337, respectively in order of appearance.

Please delete the paragraph on page 10, lines 9-11, and replace it with the following paragraph:

FIGURE 7 contains TABLE 2, which provides the results of several bioinformatic analyses relating to UDP-N-acetylmuramoylalanine-D-glutamate ligase (*murD*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 24-26, respectively in order of appearance.

Please delete the paragraph on page 11, lines 18-20, and replace it with the following paragraph:

FIGURE 20 contains TABLE 3, which provides among other things a variety of data and other information on UDP-N-acetylmuramate-alanine ligase (*murC*) from *S. aureus*. The primers are disclosed as SEQ ID NOS 33-42, and the peptides are disclosed as SEQ ID NOS 338-345, respectively in order of appearance.

Please delete the paragraph on page 11, lines 21-22, and replace it with the following paragraph:

FIGURE 21 contains TABLE 4, which provides the results of several bioinformatic analyses relating to UDP-N-acetylmuramate-alanine ligase (*murC*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 43-45, respectively in order of appearance.

Please delete the paragraph on page 13, lines 9-11, and replace it with the following paragraph:

FIGURE 38 contains TABLE 6, which provides the results of several bioinformatic analyses relating to UDP-N-acetylenolpyruvylglucosamine reductase (*murB*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 52-54, respectively in order of appearance.

Please delete the paragraph on page 14, lines 3-4, and replace it with the following paragraph:

FIGURE 47 contains TABLE 8, which provides the results of several bioinformatic analyses relating to mevalonate kinase (*mvaK1*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 61-63, respectively in order of appearance.

Please delete the paragraph on page 14, lines 28-30, and replace it with the following paragraph:

FIGURE 56 contains TABLE 10, which provides the results of several bioinformatic analyses relating to acetyl-CoA carboxylase carboxyl transferase subunit alpha (*accA*) from *E. coli*. The peptides are disclosed as SEQ ID NOS 70-72, respectively in order of appearance.

Please delete the paragraph on page 15, lines 17-19, and replace it with the following paragraph:

FIGURE 63 contains TABLE 12, which provides the results of several bioinformatic analyses relating to acetyl-CoA carboxylase carboxyl transferase subunit alpha (*accA*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 79-81, respectively in order of appearance.

Please delete the paragraph on page 16, lines 11-13, and replace it with the following paragraph:

FIGURE 72 contains TABLE 14, which provides the results of several bioinformatic analyses relating to phosphoglucosamine-mutase (*glmM (femD)*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 88-90, respectively in order of appearance.

Please delete the paragraph on page 17, lines 1-2, and replace it with the following paragraph:

FIGURE 80 contains TABLE 16, which provides the results of several bioinformatic analyses relating to D-alanine-D-alanine ligase A (*ddlA*) from *S. pneumoniae*. The peptides are disclosed as SEQ ID NOS 97-99, respectively in order of appearance.

Please delete the paragraph on page 17, lines 20-22, and replace it with the following paragraph:

FIGURE 86 contains TABLE 17, which provides among other things a variety of data and other information on phosphoglucomutase/phosphomannomutase family protein (*glmM*) from *S. pneumoniae*. The primers are disclosed as SEQ ID NOS 106-115, and the peptides are disclosed as SEQ ID NOS 346-353, respectively in order of appearance.

Please delete the paragraph on page 17, lines 23-25, and replace it with the following paragraph:

FIGURE 87 contains TABLE 18, which provides the results of several bioinformatic analyses relating to phosphoglucomutase/phosphomannomutase family protein (*glmM*) from *S. pneumoniae*. The peptides are disclosed as SEQ ID NOS 116-118, respectively in order of appearance.

Please delete the paragraph on page 19, lines 15-17, and replace it with the following paragraph:

FIGURE 103 contains TABLE 19, which provides among other things a variety of data and other information on UDP-N-acetylmuramoylalanine-D-glutamate ligase (*murD*) from *S. pneumoniae*. The primers are disclosed as SEQ ID NOS 125-135, and the peptides are disclosed as SEQ ID NOS 354-362, respectively in order of appearance.

Please delete the paragraph on page 19, lines 18-20, and replace it with the following paragraph:

FIGURE 104 contains TABLE 20, which provides the results of several bioinformatic analyses relating to UDP-N-acetyl muramoylalanine-D-glutamate ligase (*murD*) from *S. pneumoniae*. The peptides are disclosed as SEQ ID NOS 136-138, respectively in order of appearance.

Please delete the paragraph on page 20, lines 18-19, and replace it with the following paragraph:

FIGURE 115 contains TABLE 22, which provides the results of several bioinformatic analyses relating to methionyl-tRNA synthetase (*metG*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 145-147, respectively in order of appearance.

Please delete the paragraph on page 21, lines 8-9, and replace it with the following paragraph:

FIGURE 123 contains TABLE 24, which provides the results of several bioinformatic analyses relating to tyrosyl-tRNA synthetase (*tyrS*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 154-156, respectively in order of appearance.

Please delete the paragraph on page 21, lines 29-30, and replace it with the following paragraph:

FIGURE 131 contains TABLE 26, which provides the results of several bioinformatic analyses relating to histidyl-tRNA synthetase (*hisS*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 163-165, respectively in order of appearance.

Please delete the paragraph on page 22, lines 18-19, and replace it with the following paragraph:

FIGURE 139 contains TABLE 28, which provides the results of several bioinformatic analyses relating to thymidylate kinase (*tmk*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 172-174, respectively in order of appearance.

Please delete the paragraph on page 23, lines 8-9, and replace it with the following paragraph:

FIGURE 148 contains TABLE 30, which provides the results of several bioinformatic analyses relating to peptide chain release factor RF-1 (*prfA*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 181-183, respectively in order of appearance.

Please delete the paragraph on page 23, lines 29-30, and replace it with the following paragraph:

FIGURE 156 contains TABLE 32, which provides the results of several bioinformatic analyses relating to histidine tRNA synthetase (*hisS*) from *S. pneumoniae*. The peptides are disclosed as SEQ ID NOS 190-192, respectively in order of appearance.

Please delete the paragraph on page 24, lines 18-19, and replace it with the following paragraph:

FIGURE 164 contains TABLE 34, which provides the results of several bioinformatic analyses relating to BirA bifunctional protein (*birA*) from *S. pneumoniae*. The peptides are disclosed as SEQ ID NOS 199-201, respectively in order of appearance.

Please delete the paragraph on page 25, lines 9-11, and replace it with the following paragraph:

FIGURE 173 contains TABLE 36, which provides the results of several bioinformatic analyses relating to putative PTS system enzyme II A component (*usg*) from *S. pneumoniae*. The peptides are disclosed as SEQ ID NOS 208-210, respectively in order of appearance.

Please delete the paragraph on page 25, lines 31-32, and replace it with the following paragraph:

FIGURE 181 contains TABLE 37, which provides the results of several bioinformatic analyses relating to adenine phosphoribosyltransferase (*apt*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 217-219, respectively in order of appearance.

Please delete the paragraph on page 26, lines 22-23, and replace it with the following paragraph:

FIGURE 190 contains TABLE 39, which provides the results of several bioinformatic analyses relating to uridylate kinase (*pyrH*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 226-228, respectively in order of appearance.

Please delete the paragraph on page 27, lines 11-12, and replace it with the following paragraph:

FIGURE 198 contains TABLE 41, which provides the results of several bioinformatic analyses relating to guanylate kinase (*gmk*) from *S. pneumoniae*. The peptides are disclosed as SEQ ID NOS 235-237, respectively in order of appearance.

Please delete the paragraph on page 28, lines 1-3, and replace it with the following paragraph:

FIGURE 207 contains TABLE 43, which provides the results of several bioinformatic analyses relating to adenine phosphoribosyltransferase (*apt*) from *S. pneumoniae*. The peptides are disclosed as SEQ ID NOS 244-246, respectively in order of appearance.

Please delete the paragraph on page 28, lines 27-28, and replace it with the following paragraph:

FIGURE 216 contains TABLE 44, which provides among other things a variety of data and other information on uridylate kinase (*pyrH*) from *S. pneumoniae*. The primers are disclosed as SEQ ID NOS 253-265, and the peptides are disclosed as SEQ ID NOS 363-372, respectively in order of appearance.

Please delete the paragraph on page 28, lines 29-30, and replace it with the following paragraph:

FIGURE 217 contains TABLE 45, which provides the results of several bioinformatic analyses relating to uridylate kinase (*pyrH*) from *S. pneumoniae*. The peptides are disclosed as SEQ ID NOS 266-268, respectively in order of appearance.

Please delete the paragraph on page 30, lines 18-19, and replace it with the following paragraph:

FIGURE 236 contains TABLE 47, which provides the results of several bioinformatic analyses relating to uridylate kinase (*pyrH*) from *P. aeruginosa*. The peptides are disclosed as SEQ ID NOS 275-277, respectively in order of appearance.

Please delete the paragraph on page 31, lines 8-9, and replace it with the following paragraph:

FIGURE 245 contains TABLE 49, which provides the results of several bioinformatic analyses relating to phosphoglycerate kinase (*pgk*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 284-286, respectively in order of appearance.

Please delete the paragraph on page 31, lines 29-31, and replace it with the following paragraph:

FIGURE 252 contains TABLE 51, which provides the results of several bioinformatic analyses relating to flavoprotein affecting synthesis of DNA and pantothenate (*dfp*) from *E. coli*. The peptides are disclosed as SEQ ID NOS 293-295, respectively in order of appearance.

Please delete the paragraph on page 32, lines 16-17, and replace it with the following paragraph:

FIGURE 259 contains TABLE 53, which provides the results of several bioinformatic analyses relating to riboflavin kinase/FAD synthase (*ribC*) from *S. aureus*. The peptides are disclosed as SEQ ID NOS 302-304, respectively in order of appearance.

Please delete the paragraph on page 33, lines 4-6, and replace it with the following paragraph:

FIGURE 266 contains TABLE 55, which provides the results of several bioinformatic analyses relating to phosphopantetheine adenylyltransferase (*coAD*) from *P. aeruginosa*. The peptides are disclosed as SEQ ID NOS 311-313, respectively in order of appearance.

Please delete the paragraph on page 33, lines 24-25, and replace it with the following paragraph:

FIGURE 273 contains TABLE 57, which provides the results of several bioinformatic analyses relating to peptide chain release factor 1 (*prfA*) from *P. aeruginosa*. The peptides are disclosed as SEQ ID NOS 320-322, respectively in order of appearance.

Please delete the paragraph on page 69, lines 10-16, and replace it with the following paragraph:

Activation of GlmM is thought to be mediated by phosphorylation of the second serine residue within the characteristic hexophosphate mutase motif, G-V-**IM**-V-S-A-S-H-N-P (**SEQ ID NO: 323**). The GlmM homologue from *E. coli* was observed to be autophosphorylated by glucosamine 1,6-bisphosphate *in vitro*. *S. aureus* in which GlmM is inactivated is characterized by a 5% lower peptidoglycan cross-linking rate than that of the wild type enzyme, as well as a reduction of a minor component of the peptidoglycan that contains alanyl-tetraglycine instead of the lysine pentaglycine cross-linking substituent.

Please delete the paragraph on page 79, line 25, to page 80, line 6, and replace it with the following paragraph:

Dfp proteins, LanD proteins (for example EpiD, which is involved in epidermin biosynthesis), and the salt tolerance protein AtHAL3a from *Arabidopsis thaliana* are all believed to be homooligomeric flavin-containing Cys decarboxylases (HFCD protein family). The crystal structure of the peptidyl-cysteine decarboxylase EpiD complexed with a pentapeptide substrate has recently been determined at 2.5 Å resolution. The peptide is bound by an NH(2)-terminal substrate binding helix, residue Asn(117), which contacts the cysteine residue of the substrate, and a COOH-terminal substrate recognition clamp.

The conserved motif G-G/S-I-A-X-Y-K (**SEQ ID NO: 324**) of the Dfp proteins aligns partly with the substrate binding helix of EpiD. Point mutations within this motif resulted in loss of coenzyme binding (G14S) or in significant decrease of sfp activity (G15A, I16L, A17D, K20N, K20Q). Exchange of Asn(125) of Dfp, which corresponds to Asn(117) of EpiD, and exchange of Cys(158), which is within the proposed substrate recognition clamp of Dfp, led to inactivity of the enzyme. Molecular analysis of the conditional lethality of the *Escherichia coli* Dfp-707 mutant revealed that the single point mutation G11D of Dfp is related to decreased amounts of soluble Dfp protein at 37 degrees C.

Please delete the paragraph on page 163, lines 4-18, and replace it with the following paragraph:

The PCR product for each of the subject nucleic acid sequences (experimental) is directionally cloned into the polylinker region of any of three expression vectors: pET28 (Novagen), pET15 (Novagen) or pGEX (Pharmacia/LKB Biotechnology). Additional restriction enzyme sites may be engineered into the expression vectors to allow for simultaneous clones to be prepared having different purification tags. After the ligation reaction, the DNA is transformed into competent *E. coli* cells (Strains XL1-Blue (Stratagene) or DH5 α (Invitrogen)) via heat shock or electroporation as described in Sambrook, et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989). The expression vectors contain the bacteriophage T7 promoter for RNA polymerase, and the *E. coli* strain used produces T7 RNA polymerase upon induction with isopropyl- β -D-thiogalactoside (IPTG). The sequence of the cloning site adds a Glutathione S-transferase (GST) tag, or a polyhistidine (6X His) tag (**SEQ ID NO: 325**), at the N- or C- terminus of the recombinant protein. The cloning site also inserts a cleavage site for the thrombin or Tev (Invitrogen) enzymes between the recombinant protein and the N- or C- terminal GST or polyhistidine tag.

Please delete the Table on page 169, and replace it with the following Table:

<i>SEQ ID NO</i> <i>for Additional Residues</i>	<i>Additional Residues</i>	<i>Type of Tag and</i> <i>Whether or Not Removed</i>
	GSH	His tag removed from N-terminus
	MGSSHHHHHSSGLVPRGSH	His tag not removed from N-terminus

	GSEONLYFQGHHHHHH	His tag <u>not</u> removed from C-terminus
	GSEONLYFQ	His tag <u>not</u> removed from C-terminus